RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/537,897_

Source: _PCT/10_

Date Processed by STIC: _6/16/05_

ENTERED

PCT

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J537897.raw

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     5 <110> APPLICANT: CropDesign N.V.
     9 <120> TITLE OF INVENTION: Plants having modified growth characteristics and a method
for making the
    10         same
    14 <130> FILE REFERENCE: CD-070-PCT
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/537,897
C--> 18 <141> CURRENT FILING DATE: 2005-06-07
    18 <160> NUMBER OF SEQ ID NOS: 50
    22 <170> SOFTWARE: PatentIn version 3.1
    26 <210> SEQ ID NO: 1
    28 <211> LENGTH: 692
    30 <212> TYPE: DNA
    32 <213> ORGANISM: Arabidopsis thaliana
    36 <400> SEQUENCE: 1
    37 aatggcgctc gaggctctta catcaccaag attagcttct ccgattcctc ctttgttcga    60
    39 agattcttca gtcttccatg gagtcgagca ctggacaaag ggtaagcgat ctaagagatc   120
    41 aagatccgat ttccaccacc aaaacctcac tgaggaagag tatctagctt tttgcctcat   180
    43 gcttctcgct cgcgacaacc gtcagcctcc tcctcctccg gcggtggaga agttgagcta   240
    45 caagtgtagc gtctgcgaca agacgttctc ttcttaccaa gctctcggtg gtcacaaggc   300
    47 aagccaccgt aagaacttat cacagactct ctccggcgga ggagatgatc attcaacctc   360
    49 gtcggcgaca accacatccg ccgtgactac tggaagtggg aaatcacacg tttgcaccat   420
    51 ctgtaacaag tcttttcctt ccggtcaagc tctcggcgga cacaagcggt gccactacga   480
    53 aggaaacaac aacatcaaca ctagtagcgt gtccaactcc gaaggtgcgg ggtccactag   540
    55 ccacgttagc agtagccacc gtgggtttga cctcaacatc cctccgatcc ctgaattctc   600
    57 gatggtcaac ggagacgacg aagtcatgag ccctatgccg gcgaagaagc ctcggtttga   660
    59 ctttccggtc aaacttcaac tttaaggaaa tt                                  692
    62 <210> SEQ ID NO: 2
    64 <211> LENGTH: 227
    66 <212> TYPE: PRT
    68 <213> ORGANISM: Arabidopsis thaliana
    72 <400> SEQUENCE: 2
    74 Met Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro
    75 1               5                   10                  15
    78 Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr
    79             20                  25                  30
    82 Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
    83         35                  40                  45
    86 Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
    87     50                  55                  60
    90 Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
    91 65                  70                  75                  80
    94 Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
    95                 85                  90                  95
    98 Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
```

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99              100               105               110
102 Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
103         115               120               125
106 Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
107     130               135               140
110 Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
111 145               150               155               160
114 Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
115             165               170               175
118 Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
119         180               185               190
122 Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
123     195               200               205
126 Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
127     210               215               220
130 Leu Gln Leu
131 225
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136 <211> LENGTH: 50
138 <212> TYPE: DNA
140 <213> ORGANISM: Artificial sequence
144 <220> FEATURE:
146 <223> OTHER INFORMATION: primer PRM3204
148 <400> SEQUENCE: 3
149 ggggacaagt ttgtacaaaa aagcaggctt cacaatggcg ctcgaggctc              50
152 <210> SEQ ID NO: 4
154 <211> LENGTH: 53
156 <212> TYPE: DNA
158 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
164 <223> OTHER INFORMATION: primer PRM3205
166 <400> SEQUENCE: 4
167 ggggaccact ttgtacaaga aagctgggta atttccttaa agttgaagtt tga          53
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172 <211> LENGTH: 6
174 <212> TYPE: PRT
176 <213> ORGANISM: Artificial sequence
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182 <223> OTHER INFORMATION: QALGGH motif
184 <400> SEQUENCE: 5
186 Gln Ala Leu Gly Gly His
187 1               5
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192 <211> LENGTH: 6
194 <212> TYPE: PRT
196 <213> ORGANISM: Artificial sequence
200 <220> FEATURE:
202 <223> OTHER INFORMATION: NNM box
204 <220> FEATURE:
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Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J537897.raw

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         206 <221> NAME/KEY: MISC_FEATURE
         208 <222> LOCATION: (3)..(3)
         210 <223> OTHER INFORMATION: Xaa can be either methionine or tryptophan
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         217 1               5
         220 <210> SEQ ID NO: 7
         222 <211> LENGTH: 7
         224 <212> TYPE: PRT
         226 <213> ORGANISM: Artificial sequence
         230 <220> FEATURE:
         232 <223> OTHER INFORMATION: EAR motif
         234 <220> FEATURE:
         236 <221> NAME/KEY: MISC_FEATURE
         238 <222> LOCATION: (1)..(1)
         240 <223> OTHER INFORMATION: Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly,
His, I
         241        le, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)
         245 <220> FEATURE:
         247 <221> NAME/KEY: MISC_FEATURE
         249 <222> LOCATION: (5)..(5)
         251 <223> OTHER INFORMATION: Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly,
His, I
         252        le, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)
         256 <220> FEATURE:
         258 <221> NAME/KEY: MISC_FEATURE
         260 <222> LOCATION: (6)..(6)
         262 <223> OTHER INFORMATION: Xaa can be any amino acid or no amino acid
         266 <400> SEQUENCE: 7
W--> 268 Xaa Asp Leu Asn Xaa Xaa Pro
         269 1               5
         272 <210> SEQ ID NO: 8
         274 <211> LENGTH: 7
         276 <212> TYPE: PRT
         278 <213> ORGANISM: Artificial sequence
         282 <220> FEATURE:
         284 <223> OTHER INFORMATION: B-Box
         286 <220> FEATURE:
         288 <221> NAME/KEY: MISC_FEATURE
         290 <222> LOCATION: (3)..(3)
         292 <223> OTHER INFORMATION: Ser can be serine or no amino acid
         296 <220> FEATURE:
         298 <221> NAME/KEY: MISC_FEATURE
         300 <222> LOCATION: (6)..(6)
         302 <223> OTHER INFORMATION: Xaa can be any amino acid
         306 <400> SEQUENCE: 8
W--> 308 Lys Arg Ser Lys Arg Xaa Arg
         309 1               5
         312 <210> SEQ ID NO: 9
         314 <211> LENGTH: 12
         316 <212> TYPE: PRT
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  322 <220> FEATURE:
  324 <223> OTHER INFORMATION: L-Box
  326 <220> FEATURE:
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  330 <222> LOCATION: (2)..(2)
  332 <223> OTHER INFORMATION: Xaa can be any amino acid
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  338 <221> NAME/KEY: MISC_FEATURE
  340 <222> LOCATION: (4)..(5)
  342 <223> OTHER INFORMATION: Xaa can be any amino acid
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  348 <221> NAME/KEY: MISC_FEATURE
  350 <222> LOCATION: (7)..(7)
  352 <223> OTHER INFORMATION: Xaa can be any amino acid
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  358 <221> NAME/KEY: MISC_FEATURE
  360 <222> LOCATION: (10)..(11)
  362 <223> OTHER INFORMATION: Xaa can be any amino acid
  366 <400> SEQUENCE: 9
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  369 1               5                   10
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  374 <211> LENGTH: 1006
  376 <212> TYPE: DNA
  378 <213> ORGANISM: Datisca glomerata
  382 <400> SEQUENCE: 10
  383 ggcacgagga caaattctct ctctatcctc tgaatatctt tggtttgtga actgagaagc      60
  385 tattagatgg ctctagaagc gctcaactct ccgaccacag ctacgccggt gtttcactac     120
  387 gacgacccca gcttgaatta ccttgagcca tggaccaagc gtaagcgttc caagcgtacg     180
  389 cgcttagata gccccatacc gaggaagagt accttgcttt ctgcctcatc atgctcgctc     240
  391 gtggccgcgt tgcctctgca aatcgacggg attctcagtc ttccattcag attcagcctg     300
  393 aagcaacgac ttcggctacc aaagtcagtt ataagtgctc tgtgtgcgat aaggcctttt     360
  395 cgtcttatca ggctttgggt gggcacaagg ccagccacag aaagctcgct ggcggcgaag     420
  397 atcaatcgac ttcctttgcc accacgaatt cagccaccgt cactaccacc acagcctccg     480
  399 gaggtggtgg caggtctcat gagtgttcta tttgccacaa atcgttcccg actggccagg     540
  401 ccttgggtgg tcacaagcgc tgccactacg aaggcagtat cggcggcaat agtattcacc     600
  403 accacaacaa taccaccaac agcggaagca acggtggcat gagcatgacc tccgaagtag     660
  405 gttccacaca cacagtcagc cacagtcacc gtgacttcga tctcaacatc ccggccttgc     720
  407 cggagtttcg gtcgaatttc ttcatatccg gggatgacga ggtcgagagt cctcatccgg     780
  409 ccaagaaacc ccgtatattg atgaaataaa acatttctca agatcactga accaggcttt     840
  411 agtttcttta taggaggaga tttaaaaaag tagtatctct ctttctttat ccgtaggata     900
  413 attaatatat ttcgtgtaca taaatttgta gttctttaac acactctgtt tcattttctt     960
  415 gctttgctca actttgtatt ggttatttca ttatgaaaat tcaatt                   1006
  418 <210> SEQ ID NO: 11
  420 <211> LENGTH: 247
  422 <212> TYPE: PRT
  424 <213> ORGANISM: Datisca glomerata
  428 <400> SEQUENCE: 11
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RAW SEQUENCE LISTING   DATE: 06/16/2005
PATENT APPLICATION: US/10/537,897   TIME: 10:21:25

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J537897.raw**

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430 Met Ala Leu Glu Ala Leu Asn Ser Pro Thr Thr Ala Thr Pro Val Phe
431 1                   5                   10                  15
434 His Tyr Asp Asp Pro Ser Leu Asn Tyr Leu Glu Pro Trp Thr Lys Arg
435             20                  25                  30
438 Lys Arg Ser Lys Arg Thr Arg Leu Asp Ser Pro His Thr Glu Glu Glu
439         35                  40                  45
442 Tyr Leu Ala Phe Cys Leu Ile Met Leu Ala Arg Gly Arg Val Ala Ser
443     50                  55                  60
446 Ala Asn Arg Arg Asp Ser Gln Ser Ser Ile Gln Ile Gln Pro Glu Ala
447 65                  70                  75                  80
450 Thr Thr Ser Ala Thr Lys Val Ser Tyr Lys Cys Ser Val Cys Asp Lys
451                 85                  90                  95
454 Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
455             100                 105                 110
458 Lys Leu Ala Gly Gly Glu Asp Gln Ser Thr Ser Phe Ala Thr Thr Asn
459         115                 120                 125
462 Ser Ala Thr Val Thr Thr Thr Thr Ala Ser Gly Gly Gly Gly Arg Ser
463     130                 135                 140
466 His Glu Cys Ser Ile Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu
467 145                 150                 155                 160
470 Gly Gly His Lys Arg Cys His Tyr Glu Gly Ser Ile Gly Gly Asn Ser
471             165                 170                 175
474 Ile His His His Asn Asn Thr Thr Asn Ser Gly Ser Asn Gly Gly Met
475             180                 185                 190
478 Ser Met Thr Ser Glu Val Gly Ser Thr His Thr Val Ser His Ser His
479         195                 200                 205
482 Arg Asp Phe Asp Leu Asn Ile Pro Ala Leu Pro Glu Phe Arg Ser Asn
483     210                 215                 220
486 Phe Phe Ile Ser Gly Asp Asp Glu Val Glu Ser Pro His Pro Ala Lys
487 225                 230                 235                 240
490 Lys Pro Arg Ile Leu Met Lys
491                 245
494 <210> SEQ ID NO: 12
496 <211> LENGTH: 996
498 <212> TYPE: DNA
500 <213> ORGANISM: Glycine max
504 <400> SEQUENCE: 12
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507 ccaaacacat ggctttggaa gctctcaact caccaacaac aaccgctcca tcttttccct   120
509 ttgacgaccc aactattcca tgggcgaaac gaaaacgttc aaagcgttct cgcgaccatc   180
511 cttctgaaga agagtacctc gccctctgcc tcatcatgct cgctcgcggc ggcaccacca   240
513 ccgtcaacaa ccgccacgtc agccctccgc cgctacagcc acagccacag ccgacaccag   300
515 atccttccac caagctcagt tacaaatgct ccgtttgcga caagagcttc ccctcttacc   360
517 aagcgctcgg tggacacaag gccagtcacc ggaaactcgc cggcgccgcc gaagaccaac   420
519 cccccagcac caccacttcc tccgccgccg ccaccagctc cgcctccgga ggtaaggccc   480
521 atgagtgctc catttgccac aaatccttcc ccaccggaca ggcccttggc ggacacaaac   540
523 gttgtcacta cgaaggtaac ggtaacggaa ataacaacaa cagtaacagc gttgtcaccg   600
525 tcgcctcgga aggcgtgggc tccacccaca ctgtcagtca cggccaccac cgcgacttcg   660
527 atctcaacat cccggccttt ccggattttt cgaccaaggt cggagaagac gaggttgaga   720
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/537,897

DATE: 06/16/2005
TIME: 10:21:26

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J537897.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3
Seq#:7; Xaa Pos. 1,5,6
Seq#:8; Xaa Pos. 6
Seq#:9; Xaa Pos. 2,4,5,7,10,11
Seq#:40; N Pos. 406,581,582,589

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/537,897

DATE: 06/16/2005
TIME: 10:21:26

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J537897.raw**

```
L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:2221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:360
M:341 Repeated in SeqNo=40
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